

SEQUENCE LISTING



<110> Covacci, Antonello
Bugnoli, Massimo
Telford, John
Macchia, Giovanni
Rappuoli, Rino

<120> Helicobacter Pylori Cytotoxin Proteins Useful For
Vaccines And Diagnostics

<130> CHIR0158

<140> 09/360,934

<141> 1999-07-26

<160> 8

<170> PatentIn Ver. 2.1

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<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificial
Sequence

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27

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<211> 3960

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Artificial
Sequence

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<211> 1296

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificial Sequence

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Ala Ala Phe Phe Thr Thr Val Ile Ile Pro Ala Ile Val Gly Gly Ile
 35 40 45

Ala Thr Gly Thr Ala Val Gly Thr Val Ser Gly Leu Leu Ser Trp Gly
 50 55 60

Leu Lys Gln Ala Glu Glu Ala Asn Lys Thr Pro Asp Lys Pro Asp Lys
 65 70 75 80

Val Trp Arg Ile Gln Ala Gly Lys Gly Phe Asn Glu Phe Pro Asn Lys
 85 90 95

Glu Tyr Asp Leu Tyr Arg Ser Leu Leu Ser Ser Lys Ile Asp Gly Gly
 100 105 110

Trp Asp Trp Gly Asn Ala Ala Arg His Tyr Trp Val Lys Gly Gly Gln
 115 120 125

Gln Asn Lys Leu Glu Val Asp Met Lys Asp Ala Val Gly Thr Tyr Thr
 130 135 140
 Leu Ser Gly Leu Arg Asn Phe Thr Gly Gly Asp Leu Asp Val Asn Met
 145 150 155 160
 Gln Lys Ala Thr Leu Arg Leu Gly Gln Phe Asn Gly Asn Ser Phe Thr
 165 170 175
 Ser Tyr Lys Asp Ser Ala Asp Arg Thr Thr Arg Val Asp Phe Asn Ala
 180 185 190
 Lys Asn Ile Ser Ile Asp Asn Phe Val Glu Ile Asn Asn Arg Val Gly
 195 200 205
 Ser Gly Ala Gly Arg Lys Ala Ser Ser Thr Val Leu Thr Leu Gln Ala
 210 215 220
 Ser Glu Gly Ile Thr Ser Asp Lys Asn Ala Glu Ile Ser Leu Tyr Asp
 225 230 235 240
 Gly Ala Thr Leu Asn Leu Ala Ser Ser Ser Val Lys Leu Met Gly Asn
 245 250 255
 Val Trp Met Gly Arg Leu Gln Tyr Val Gly Ala Tyr Leu Ala Pro Ser
 260 265 270
 Tyr Ser Thr Ile Asn Thr Ser Lys Val Thr Gly Glu Val Asn Phe Asn
 275 280 285
 His Leu Thr Val Gly Asp Lys Asn Ala Ala Gln Ala Gly Ile Ile Ala
 290 295 300
 Asn Lys Lys Thr Asn Ile Gly Thr Leu Asp Leu Trp Gln Ser Ala Gly
 305 310 315 320
 Leu Asn Ile Ile Ala Pro Pro Glu Gly Gly Tyr Lys Asp Lys Pro Asn
 325 330 335
 Asn Thr Pro Ser Gln Ser Gly Ala Lys Asn Asp Lys Asn Glu Ser Ala
 340 345 350
 Lys Asn Asp Lys Gln Glu Ser Ser Gln Asn Asn Ser Asn Thr Gln Val
 355 360 365
 Ile Asn Pro Pro Asn Ser Ala Gln Lys Thr Glu Val Gln Pro Thr Gln
 370 375 380

Val Ile Asp Gly Pro Phe Ala Gly Gly Lys Asp Thr Val Val Asn Ile
385 390 395 400
Asn Arg Ile Asn Thr Asn Ala Asp Gly Thr Ile Arg Val Gly Gly Phe
405 410 415
Lys Ala Ser Leu Thr Thr Asn Ala Ala His Leu His Ile Gly Lys Gly
420 425 430
Gly Val Asn Leu Ser Asn Gln Ala Ser Gly Arg Ser Leu Ile Val Glu
435 440 445
Asn Leu Thr Gly Asn Ile Thr Val Asp Gly Pro Leu Arg Val Asn Asn
450 455 460
Gln Val Gly Gly Tyr Ala Leu Ala Gly Ser Ser Ala Asn Phe Glu Phe
465 470 475 480
Lys Ala Gly Thr Asp Thr Lys Asn Gly Thr Ala Thr Phe Asn Asn Asp
485 490 495
Ile Ser Leu Gly Arg Phe Val Asn Leu Lys Val Asp Ala His Thr Ala
500 505 510
Asn Phe Lys Gly Ile Asp Thr Gly Asn Gly Gly Phe Asn Thr Leu Asp
515 520 525
Phe Ser Gly Val Thr Asp Lys Val Asn Ile Asn Lys Leu Ile Thr Ala
530 535 540
Ser Thr Asn Val Ala Val Lys Asn Phe Asn Ile Asn Glu Leu Ile Val
545 550 555 560
Lys Thr Asn Gly Ile Ser Val Gly Glu Tyr Thr His Phe Ser Glu Asp
565 570 575
Ile Gly Ser Gln Ser Arg Ile Asn Thr Val Arg Leu Glu Thr Gly Thr
580 585 590
Arg Ser Leu Phe Ser Gly Gly Val Lys Phe Lys Gly Gly Glu Lys Leu
595 600 605
Val Ile Asp Glu Phe Tyr Tyr Ser Pro Trp Asn Tyr Phe Asp Ala Arg
610 615 620
Asn Ile Lys Asn Val Glu Ile Thr Asn Lys Leu Ala Phe Gly Pro Gln
625 630 635 640

Gly	Ser	Pro	Trp	Gly	Thr	Ser	Lys	Leu	Met	Phe	Asn	Asn	Leu	Thr	Leu	645	650	655	
Gly	Gln	Asn	Ala	Val	Met	Asp	Tyr	Ser	Gln	Phe	Ser	Asn	Leu	Thr	Ile	660	665	670	
Gln	Gly	Asp	Phe	Ile	Asn	Asn	Gln	Gly	Thr	Ile	Asn	Tyr	Leu	Val	Arg	675	680	685	
Gly	Gly	Lys	Val	Ala	Thr	Leu	Ser	Val	Gly	Asn	Ala	Ala	Ala	Met	Met	690	695	700	
Phe	Asn	Asn	Asp	Ile	Asp	Ser	Ala	Thr	Gly	Phe	Tyr	Lys	Pro	Leu	Ile	705	710	715	720
Lys	Ile	Asn	Ser	Ala	Gln	Asp	Leu	Ile	Lys	Asn	Thr	Glu	His	Val	Leu	725	730	735	
Leu	Lys	Ala	Lys	Ile	Ile	Gly	Tyr	Gly	Asn	Val	Ser	Thr	Gly	Thr	Asn	740	745	750	
Gly	Ile	Ser	Asn	Val	Asn	Leu	Glu	Glu	Gln	Phe	Lys	Glu	Arg	Leu	Ala	755	760	765	
Leu	Tyr	Asn	Asn	Asn	Asn	Arg	Met	Asp	Thr	Cys	Val	Val	Arg	Asn	Thr	770	775	780	
Asp	Asp	Ile	Lys	Ala	Cys	Gly	Met	Ala	Ile	Gly	Asp	Gln	Ser	Met	Val	785	790	795	800
Asn	Asn	Pro	Asp	Asn	Tyr	Lys	Tyr	Leu	Ile	Gly	Lys	Ala	Trp	Lys	Asn	805	810	815	
Ile	Gly	Ile	Ser	Lys	Thr	Ala	Asn	Gly	Ser	Lys	Ile	Ser	Val	Tyr	Tyr	820	825	830	
Leu	Gly	Asn	Ser	Thr	Pro	Thr	Glu	Asn	Gly	Gly	Asn	Thr	Thr	Asn	Leu	835	840	845	
Pro	Thr	Asn	Thr	Thr	Ser	Asn	Ala	Arg	Ser	Ala	Asn	Asn	Ala	Leu	Ala	850	855	860	
Gln	Asn	Ala	Pro	Phe	Ala	Gln	Pro	Ser	Ala	Thr	Pro	Asn	Leu	Val	Ala	865	870	875	880
Ile	Asn	Gln	His	Asp	Phe	Gly	Thr	Ile	Glu	Ser	Val	Phe	Glu	Leu	Ala	885	890	895	

Asn Arg Ser Lys Asp Ile Asp Thr Leu Tyr Ala Asn Ser Gly Ala Gln		
900	905	910
Gly Arg Asp Leu Leu Gln Thr Leu Leu Ile Asp Ser His Asp Ala Gly		
915	920	925
Tyr Ala Arg Lys Met Ile Asp Ala Thr Ser Ala Asn Glu Ile Thr Lys		
930	935	940
Gln Leu Asn Thr Ala Thr Thr Thr Leu Asn Asn Ile Ala Ser Leu Glu		
945	950	955 960
His Lys Thr Ser Gly Leu Gln Thr Leu Ser Leu Ser Asn Ala Met Ile		
965	970	975
Leu Asn Ser Arg Leu Val Asn Leu Ser Arg Arg His Thr Asn His Ile		
980	985	990
Asp Ser Phe Ala Lys Arg Leu Gln Ala Leu Lys Asp Gln Lys Phe Ala		
995	1000	1005
Ser Leu Glu Ser Ala Ala Glu Val Leu Tyr Gln Phe Ala Pro Lys Tyr		
1010	1015	1020
Glu Lys Pro Thr Asn Val Trp Ala Asn Ala Ile Gly Gly Thr Ser Leu		
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Asn Asn Gly Ser Asn Ala Ser Leu Tyr Gly Thr Ser Ala Gly Val Asp		
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Ala Tyr Leu Asn Gly Gln Val Glu Ala Ile Val Gly Gly Phe Gly Ser		
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Tyr Gly Tyr Ser Ser Phe Asn Asn Arg Ala Asn Ser Leu Asn Ser Gly		
1075	1080	1085
Ala Asn Asn Thr Asn Phe Gly Val Tyr Ser Arg Ile Phe Ala Asn Gln		
1090	1095	1100
His Glu Phe Asp Phe Glu Ala Gln Gly Ala Leu Gly Ser Asp Gln Ser		
1105	1110	1115 1120
Ser Leu Asn Phe Lys Ser Ala Leu Leu Gln Asp Leu Asn Gln Ser Tyr		
1125	1130	1135
His Tyr Leu Ala Tyr Ser Ala Ala Thr Arg Ala Ser Tyr Gly Tyr Asp		
1140	1145	1150

Phe Ala Phe Phe Arg Asn Ala Leu Val Leu Lys Pro Ser Val Gly Val
 1155 1160 1165

Ser Tyr Asn His Leu Gly Ser Thr Asn Phe Lys Ser Asn Ser Thr Asn
 1170 1175 1180

Gln Val Ala Leu Lys Asn Gly Ser Ser Ser Gln His Leu Phe Asn Ala
 1185 1190 1195 1200

Ser Ala Asn Val Glu Ala Arg Tyr Tyr Tyr Gly Asp Thr Ser Tyr Phe
 1205 1210 1215

Tyr Met Asn Ala Gly Val Leu Gln Glu Phe Ala His Val Gly Ser Asn
 1220 1225 1230

Asn Ala Ala Ser Leu Asn Thr Phe Lys Val Asn Ala Ala Arg Asn Pro
 1235 1240 1245

Leu Asn Thr His Ala Arg Val Met Met Gly Gly Glu Leu Lys Leu Ala
 1250 1255 1260

Lys Glu Val Phe Leu Asn Leu Gly Val Val Tyr Leu His Asn Leu Ile
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Ser Asn Ile Gly His Phe Ala Ser Asn Leu Gly Met Arg Tyr Ser Phe
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<211> 5925

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificial
 Sequence

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<210> 5

<211> 1147

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificial
Sequence

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Asp	Asn	Ala	Val	Ala	Ser	Tyr	Asp	Pro	Asp	Gln	Lys	Pro	Ile	Val	Asp
		35					40					45			

Lys	Asn	Asp	Arg	Asp	Asn	Arg	Gln	Ala	Phe	Glu	Gly	Ile	Ser	Gln	Leu
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Arg	Glu	Glu	Tyr	Ser	Asn	Lys	Ala	Ile	Lys	Asn	Pro	Thr	Lys	Lys	Asn
65					70					75					80

Gln	Tyr	Phe	Ser	Asp	Phe	Ile	Asn	Lys	Ser	Asn	Asp	Leu	Ile	Asn	Lys
				85					90					95	

Asp	Asn	Leu	Ile	Asp	Val	Glu	Ser	Ser	Thr	Lys	Ser	Phe	Gln	Lys	Phe
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Gly	Asp	Gln	Arg	Tyr	Arg	Ile	Phe	Thr	Ser	Trp	Val	Ser	His	Gln	Asn
	115						120					125			

Asp	Pro	Ser	Lys	Ile	Asn	Thr	Arg	Ser	Ile	Arg	Asn	Phe	Met	Glu	Asn
	130					135					140				

Ile	Ile	Gln	Pro	Pro	Ile	Leu	Asp	Asp	Lys	Glu	Lys	Ala	Glu	Phe	Leu
145					150					155					160

Lys	Ser	Ala	Lys	Gln	Ser	Phe	Ala	Gly	Ile	Ile	Ile	Gly	Asn	Gln	Ile
			165						170					175	

Arg	Thr	Asp	Gln	Lys	Phe	Met	Gly	Val	Phe	Asp	Glu	Ser	Leu	Lys	Glu
		180						185					190		

Arg	Gln	Glu	Ala	Glu	Lys	Asn	Gly	Glu	Pro	Thr	Gly	Gly	Asp	Trp	Leu
	195						200					205			

Asp	Ile	Phe	Leu	Ser	Phe	Ile	Phe	Asp	Lys	Lys	Gln	Ser	Ser	Asp	Val	210	215	220	
Lys	Glu	Ala	Ile	Asn	Gln	Glu	Pro	Val	Pro	His	Val	Gln	Pro	Asp	Ile	225	230	235	240
Ala	Thr	Thr	Thr	Thr	Asp	Ile	Gln	Gly	Leu	Pro	Pro	Glu	Ala	Arg	Asp	245	250	255	
Leu	Leu	Asp	Glu	Arg	Gly	Asn	Phe	Ser	Lys	Phe	Thr	Leu	Gly	Asp	Met	260	265	270	
Glu	Met	Leu	Asp	Val	Glu	Gly	Val	Ala	Asp	Ile	Asp	Pro	Asn	Tyr	Lys	275	280	285	
Phe	Asn	Gln	Leu	Leu	Ile	His	Asn	Asn	Ala	Leu	Ser	Ser	Val	Leu	Met	290	295	300	
Gly	Ser	His	Asn	Gly	Ile	Glu	Pro	Glu	Lys	Val	Ser	Leu	Leu	Tyr	Gly	305	310	315	320
Gly	Asn	Gly	Gly	Pro	Gly	Ala	Arg	His	Asp	Trp	Asn	Ala	Thr	Val	Gly	325	330	335	
Tyr	Lys	Asp	Gln	Gln	Gly	Asn	Asn	Val	Ala	Thr	Ile	Ile	Asn	Val	His	340	345	350	
Met	Lys	Asn	Gly	Ser	Gly	Leu	Val	Ile	Ala	Gly	Gly	Glu	Lys	Gly	Ile	355	360	365	
Asn	Asn	Pro	Ser	Phe	Tyr	Leu	Tyr	Lys	Glu	Asp	Gln	Leu	Thr	Gly	Ser	370	375	380	
Gln	Arg	Ala	Leu	Ser	Gln	Glu	Glu	Ile	Gln	Asn	Lys	Ile	Asp	Phe	Met	385	390	395	400
Glu	Phe	Leu	Ala	Gln	Asn	Asn	Ala	Lys	Leu	Asp	Asn	Leu	Ser	Glu	Lys	405	410	415	
Glu	Lys	Glu	Lys	Phe	Arg	Thr	Glu	Ile	Lys	Asp	Phe	Gln	Lys	Asp	Ser	420	425	430	
Lys	Ala	Tyr	Leu	Asp	Ala	Leu	Gly	Asn	Asp	Arg	Ile	Ala	Phe	Val	Ser	435	440	445	
Lys	Lys	Asp	Thr	Lys	His	Ser	Ala	Leu	Ile	Thr	Glu	Phe	Gly	Asn	Gly	450	455	460	

Asp	Leu	Ser	Tyr	Thr	Leu	Lys	Asp	Tyr	Gly	Lys	Lys	Ala	Asp	Lys	Ala	
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Leu	Asp	Arg	Glu	Lys	Asn	Val	Thr	Leu	Gln	Gly	Ser	Leu	Lys	His	Asp	
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Gly	Val	Met	Phe	Val	Asp	Tyr	Ser	Asn	Phe	Lys	Tyr	Thr	Asn	Ala	Ser	
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Glu	Val	Gly	Phe	Asn	Lys	Val	Ala	Ile	Phe	Asn	Leu	Pro	Asp	Leu	Asn	
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Thr	Thr	Lys	Gly	Leu	Ser	Pro	Gln	Glu	Ala	Asn	Lys	Leu	Ile	Lys	Asp	
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Lys	Ala	Val	Ala	Asp	Ala	Lys	Asn	Thr	Gly	Asn	Tyr	Asp	Glu	Val	Lys	
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Lys	Ala	Gln	Lys	Asp	Leu	Glu	Lys	Ser	Leu	Arg	Lys	Arg	Glu	His	Leu	
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Glu	Lys	Glu	Val	Glu	Lys	Lys	Leu	Glu	Ser	Lys	Ser	Gly	Asn	Lys	Asn	
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Asn	Val	Asn	Lys	Asn	Leu	Lys	Asp	Phe	Asp	Lys	Ser	Phe	Asp	Glu	Phe	
	690					695					700					
Lys	Asn	Gly	Lys	Asn	Lys	Asp	Phe	Ser	Lys	Ala	Glu	Glu	Thr	Leu	Lys	
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Ala	Leu	Lys	Gly	Ser	Val	Lys	Asp	Leu	Gly	Ile	Asn	Pro	Glu	Trp	Ile		
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Ser	Lys	Val	Glu	Asn	Leu	Asn	Ala	Ala	Leu	Asn	Glu	Phe	Lys	Asn	Gly		
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Asn	Ser	Val	Lys	Asp	Val	Ile	Ile	Asn	Gln	Lys	Val	Thr	Asp	Lys	Val		
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Asp	Asn	Leu	Asn	Gln	Ala	Val	Ser	Val	Ala	Lys	Ala	Thr	Gly	Asp	Phe		
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Ser	Arg	Val	Glu	Gln	Ala	Leu	Ala	Asp	Leu	Lys	Asn	Phe	Ser	Lys	Glu		
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Gln	Leu	Ala	Gln	Gln	Ala	Gln	Lys	Asn	Glu	Ser	Leu	Asn	Ala	Arg	Lys		
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Lys	Ser	Glu	Ile	Tyr	Gln	Ser	Val	Lys	Asn	Gly	Val	Asn	Gly	Thr	Leu		
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Val	Gly	Asn	Gly	Leu	Ser	Gln	Ala	Glu	Ala	Thr	Thr	Leu	Ser	Lys	Asn		
	850					855					860						
Phe	Ser	Asp	Ile	Lys	Lys	Glu	Leu	Asn	Ala	Lys	Leu	Gly	Asn	Phe	Asn		
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Ala	Gln	Val	Ala	Lys	Lys	Val	Asn	Ala	Lys	Ile	Asp	Arg	Leu	Asn	Gln		
		915					920					925					
Ile	Ala	Ser	Gly	Leu	Gly	Val	Val	Gly	Gln	Ala	Ala	Gly	Phe	Pro	Leu		
	930					935					940						
Lys	Arg	His	Asp	Lys	Val	Asp	Asp	Leu	Ser	Lys	Val	Gly	Leu	Ser	Arg		
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Glu Ala Lys Ala Gly Phe Phe Gly Asn Leu Glu Gln Thr Ile Asp Lys
980 985 990

Leu Lys Asp Ser Thr Lys His Asn Pro Met Asn Leu Trp Val Glu Ser
995 1000 1005

Ala Lys Lys Val Pro Ala Ser Leu Ser Ala Lys Leu Asp Asn Tyr Ala
1010 1015 1020

Thr Asn Ser His Ile Arg Ile Asn Ser Asn Ile Lys Asn Gly Ala Ile
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Asn Glu Lys Ala Thr Gly Met Leu Thr Gln Lys Asn Pro Glu Trp Leu
1045 1050 1055

Lys Leu Val Asn Asp Lys Ile Val Ala His Asn Val Gly Ser Val Pro
1060 1065 1070

Leu Ser Glu Tyr Asp Lys Ile Gly Phe Asn Gln Lys Asn Met Lys Asp
1075 1080 1085

Tyr Ser Asp Ser Phe Lys Phe Ser Thr Lys Leu Asn Asn Ala Val Lys
1090 1095 1100

Asp Thr Asn Ser Gly Phe Thr Gln Phe Leu Thr Asn Ala Phe Ser Thr
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<210> 6

<211> 546

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificial
Sequence

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 290 295 300
 Gly Leu Ser Leu Glu Asn Ala Glu Val Glu Phe Leu Gly Lys Ala Gly
 305 310 315 320
 Arg Ile Val Ile Asp Lys Asp Asn Thr Thr Ile Val Asp Gly Lys Gly
 325 330 335
 His Ser Asp Asp Val Lys Asp Arg Val Ala Gln Ile Lys Thr Gln Ile
 340 345 350
 Ala Ser Thr Thr Ser Asp Tyr Asp Lys Glu Lys Leu Gln Glu Arg Leu
 355 360 365
 Ala Lys Leu Ser Gly Gly Val Ala Val Ile Lys Val Gly Ala Ala Ser
 370 375 380
 Glu Val Glu Met Lys Glu Lys Lys Asp Arg Val Asp Asp Ala Leu Ser
 385 390 395 400
 Ala Thr Lys Ala Ala Val Glu Glu Gly Ile Val Ile Gly Gly Gly Ala
 405 410 415
 Ala Leu Ile Arg Ala Ala Gln Lys Val His Leu Asn Leu His Asp Asp
 420 425 430
 Glu Lys Val Gly Tyr Glu Ile Ile Met Arg Ala Ile Lys Ala Pro Leu
 435 440 445
 Ala Gln Ile Ala Ile Asn Ala Gly Tyr Asp Gly Gly Val Val Val Asn
 450 455 460
 Glu Val Glu Lys His Glu Gly His Phe Gly Phe Asn Ala Ser Asn Gly
 465 470 475 480
 Lys Tyr Val Asp Met Phe Lys Glu Gly Ile Ile Asp Pro Leu Lys Val
 485 490 495
 Glu Arg Ile Ala Leu Gln Asn Ala Val Ser Val Ser Ser Leu Leu Leu
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530

535

540

Met Met

545

<210> 7

<211> 1838

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificial
Sequence

<400> 7

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<211> 18
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificial
Sequence

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18

B1
cont